Results: We tested 3,921 stool samples and identified 170 patients with CDI (1.04 cases per 10,000 patient-days). Seventy-eight of the CDI patients were treated with MNZ and 41 were treated with VCM. No significant demographic or clinical differences were found between the two groups. The 90-day all-cause mortality rates in the MNZ and VCM groups were 16.2% and 28.9%, respectively. The survival curves did not differ significantly between the two groups after adjusting for several confounders established to be independent risk factors for severe or complicated-course CDI (age, hypoalbuminemia, acute kidney injuries, leukocytosis, hypotension or shock).

Conclusion: Our study, Japan's first multi-center assessment of CDI treatment, showed no significant difference in prognosis between the MNZ group and VCM group. We expect MNZ to become a drug of choice for the treatment of CDI.

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Clinical profile, susceptibility patterns, treatment and outcomes of melioidosis in India

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Background: Melioidosis, caused by *Burkholderia pseudomallei*, is endemic to India and has been associated with significant morbidity and mortality. Since it mimics several other diseases, it is grossly under-recognised. This study was undertaken to describe the clinical manifestations, drugsusceptibility and outcomes of melioidosis in India.

Methods & Materials: We carried out a retrospective study of adult patients admitted with culture proven melioidosis ina tertiary care hospital in South India from 2008 to 2014.

Results: 114 patients, with a mean age of 45 years (92% males) were included. The patients were from 15 states, majority being from West Bengal (26.3%), Jharkhand (22.8%) and Tamil Nadu (14.9%). Common risk factors included diabetes (82.3%), and alcoholism (14%). The mean duration of symptoms, commonly fever, was 4 months and majority (78%) had multifocal disease. Patients presented in the cooler months (80.5%), especially in the acute group. Chronic melioidosis was commoner than acute disease (64% vs 36%). 11 patients (15%) among chronic melioidosis presented with an acute worsening and bacteremia. Bacteremia (80% vs 41%) and respiratory involvement (39% vs 16%) were more common in acute disease. Chronic granulomatous disease was associated with splenic (50% vs 29%), genitourinary (17.8 vs 4.9%) and bone involvement (12.3 vs 7%). Drug susceptibility to Carbepenems was 100%, Ceftazidime 98.1% while resistance to Trimethoprim-Sulfamethoxazole and Doxycycline was 5.9% and 2.6%. Our patients received induction therapy with Ceftazidime or Meropenem followed by eradication treatment with Trimethoprim-Sulfamethoxazole and Doxycycline. 50.9% patients required a surgical intervention and 21.9% were admitted to an intensive care unit. The case fatality rate was 14.9%. Bacteremia ($p < 0.001$) and respiratory involvement ($p = 0.003$) were associated with increased mortality. 57.9% patients were followed up and 3.5% patients had a relapse.

Conclusion: Melioidosis is an emerging infection in India. Majority of the patients are diabetics presenting with chronic granulomatous disease. Patients with septicemia and respiratory involvement had poorer outcome. A high index of suspicion in the appropriate clinical setting, and early initiation of therapy are essential.

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Emerging trends in the antibiotic susceptibility pattern of vibrio cholerae in North Karnataka

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Background: Acute diarrhoea is the second most prevalent communicable disease and a fourth leading cause of death in India with 10762500 cases and 32218 deaths reported in 2013. Cholera is an acute diarrhoeal illness caused by toxigenic strains of Vibrio cholerae serogroups O1 and O139. This study has been done with the aim of evaluating the serogroups, antimicrobial susceptibility pattern, age and gender wise distribution of Vibrio cholerae isolates from cholera epidemics in Bidar and rural parts of north Karnataka, India during the years 2008 to 2015 till date.

Methods & Materials: A total 500 stool samples of cholera outbreak from Year 2008 to 2015 till date were collected and processed at Department of Microbiology, Bidar Institute of Medical Sciences, Bidar, Karnataka, India as per the routine microbiological investigations. The isolates were identified as Vibrio cholerae and confirmed by serological tests with Polyvalent O1, O139 and mono specific Ogawa and Inaba antisera. Antibiotic sensitivity testing was done as per the CLSI guidelines.

Results: Vibrio cholerae biotype ElTor, sero group O1 grown in 155 samples (31%). Among 155 isolates obtained, of which, 136 (87.74%) were belonged to Ogawa, 13 (8.3%) belonged to Inaba and 06 (03.8%) to Hikozima. The isolates showed Multi drug resistance to Ampicillin (81.93%), Nalidixic acid (66.45%) and Ofloxacin (32.90%) throughout the study period. And Vibrio cholerae isolates showed resistance to Ciprofloxacin (22.58%), Doxycycline (14.83%) and Tetracycline (16.77%) indicating development of resistance of V. Cholerae to the drugs which are commonly used to treat Cholera infection. The infection was predominant in male and among patients age between 0-10 years (26%).

Conclusion: This is the first study conducted in the North Karnataka which reflects the importance of control and monitoring of V. cholerae by serogroup and antibiogram typing for policy makers and health professionals of this region as incidence of cholera increased year wise and changing trend in the antibiotic susceptibility pattern of V. cholerae was observed which is due to environmental factors and widespread use of antibiotics.

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Bacteriological profile of chronic osteomyelitis in a tertiary care hospital in South India

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Background: Chronic osteomyelitis (COM) is a major medical problem in most countries, mainly associated with violent trauma, modern surgery and inadequate treatment of acute osteomyelitis. Although the incidence of osteomyelitis has reduced to a certain extent with the advent of antibiotics and chemotherapeutic agents, yet it continues to be a major problem in India.

Methods & Materials: A retrospective analysis of data of purulent (Pus/pus swabs, tissue) specimen received from patients with chronic osteomyelitis by the microbiology department between January 2013-0ctober 2015 was carried out. The samples were processed using standard microbiological techniques. Identification and antimicrobial susceptibility pattern of the bacterial isolates were done using the Vitek 2 (*bioMerieux, Marcy l'Etoile- France*) system.

Results: In all, 184 patients with chronic osteomyelitis were documented during the study period. There was a male preponderance (163 / 184, 88.5%) with majority, in the age group of 10-20 years. Trauma was the major risk factor for osteomyelitis (95/ 184, 51.6%). The lower limb bones were more commonly affected of which femur (166/184, 90.2%) was the predominant bone involved. Culture was positive in 104/184 (56.6%), with the Gram positive organisms most predominant. MRSA was the predominant organism isolated in 28/104 (27%) cases. Among Gram negative bacilli, *Escherichia coli* was most common organism isolated in 11/104 (10.4%). Other organisms isolated included *Pseudomonas aeruginosa, Klebsiella pneumonia, Acinetobacter baumanii, Proteus mirabilis, Enterobacter cloacae, Morganella morgagnii* and showed a high level of antibiotic resistance. In this study no anaerobic organisms were isolated. One patient had a mixed infection with *Mycobacterium tuberculosis* and *A.baumannii.* Majority of the patients (85/184, 46%) were managed conservatively with wound care and antibiotics. No mortality was recorded.

Conclusion: Prognosis of chronic osteomyelitis depends on proper microbiological techniques that help in isolation, identification and treatment of the bone-infecting, often multidrug resistant organism. Complications can be further reduced with surgical debridement and removal of the dead tissues.

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Characterization of diarrhoegenic escherichia coli using a novel multiplex PCR

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Background: Diarrheal diseases are the second most common cause of infant mortality and morbidity in children less than five years of age. Among all the diarrheal pathogens, Diarrhoegenic *Escherichia coli* (DEC) plays an important role in epidemic and endemic diarrhea. For the identification of these pathogens, serotypic markers may correlate but are rarely reliably sufficient in identifying a strain as diarrheagenic. PCR targeting the virulence factors is a reliable and rapid way of detecting DEC. This study was undertaken to characterize DEC with diarrhea using multiplex PCR DEC and to obtain the clinico- microbiological profile of the infection.

Methods & Materials: One hundred and twenty children below 5 years of age with diarrhea attending Paediatric department were enrolled in our study after obtaining written informed consent of their parents or guardians for a period of two years from October 2013 to October 2015. Fecal samples were collected from these children. Escherichia coli isolates grown were identified by biochemical reactions. A multiplex PCR was developed to detect the virulence genes (*aggR, eaeA, bfpA, ial, lt, st, stx1* and *stx2*) of various pathotypes of DEC.

Results: Among all, 45 samples had DEC. Of them 21(49%) were Enteropatogenic *E.coli*, 6(13.3%) were Enterotoxigenic *E.coli*, 5 (11%) were Enteroaggregative *E.coli*, 4(9%) were Enterohaemorrhagic *E.coli* and 3(6.6%) were Enteroinvasive *E.coli*. We also found in our study 3(6.6%) hybrid strains (2 were atypicalEPEC and EAEC and 1 was EIEC with EHEC) and 3(6.6%) mixed infections {EAEC and EIEC, typical EPEC and EHEC, EAEC and atypical EPEC). Out of 22 EPEC positive samples, 5 (22%) were identified as atypical EPEC as they possessed *eaeA* only and not *bfpA*,3 (13.6%) isolates were identified as typical as they possessed both *eaeA* and *bfpA* genes, while 13 isolates(59%) possessed only *bfpA* gene. The majority (90%) of cases of EPEC diarrhea clustered in the less than two years age group.

Conclusion: This multiplex PCR technology will serve as a good epidemiological tool for the screening of pathotypes of DEC that causes diarrhea in children.

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